SEQUENCE LISTING

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<120> MODULATION OF GROWTH HORMONE RECEPTOR EXPRESSION AND INSULIN LIKE GROWTH FACTOR EXPRESSION

<130> BIOL0002US

<150> 60/451,455

<151> 2003-02-28

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Met Asp Leu Trp
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cag ctg ctg ttg acc ttg gca ctg gca gga tca agt gat gct ttt tct 103
Gln Leu Leu Leu Thr Leu Ala Leu Ala Gly Ser Ser Asp Ala Phe Ser
5 10 15 20

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gga agt gag gcc aca gca gct atc ctt agc aga gca ccc tgg agt ctg     151
Gly Ser Glu Ala Thr Ala Ala Ile Leu Ser Arg Ala Pro Trp Ser Leu
                 25                  30                  35

caa agt gtt aat cca ggc cta aag aca aat tct tct aag gag cct aaa     199
Gln Ser Val Asn Pro Gly Leu Lys Thr Asn Ser Ser Lys Glu Pro Lys
             40                  45                  50

ttc acc aag tgc cgt tca cct gag cga gag act ttt tca tgc cac tgg     247
Phe Thr Lys Cys Arg Ser Pro Glu Arg Glu Thr Phe Ser Cys His Trp
         55                  60                  65

aca gat gag gtt cat cat ggt aca aag aac cta gga ccc ata cag ctg     295
Thr Asp Glu Val His His Gly Thr Lys Asn Leu Gly Pro Ile Gln Leu
     70                  75                  80

ttc tat acc aga agg aac act caa gaa tgg act caa gaa tgg aaa gaa     343
Phe Tyr Thr Arg Arg Asn Thr Gln Glu Trp Thr Gln Glu Trp Lys Glu
 85                  90                  95                 100

tgc cct gat tat gtt tct gct ggg gaa aac agc tgt tac ttt aat tca     391
Cys Pro Asp Tyr Val Ser Ala Gly Glu Asn Ser Cys Tyr Phe Asn Ser
                105                 110                 115

tcg ttt acc tcc atc tgg ata cct tat tgt atc aag cta act agc aat     439
Ser Phe Thr Ser Ile Trp Ile Pro Tyr Cys Ile Lys Leu Thr Ser Asn
            120                 125                 130

ggt ggt aca gtg gat gaa aag tgt ttc tct gtt gat gaa ata gtg caa     487
Gly Gly Thr Val Asp Glu Lys Cys Phe Ser Val Asp Glu Ile Val Gln
        135                 140                 145

cca gat cca ccc att gcc ctc aac tgg act tta ctg aac gtc agt tta     535
Pro Asp Pro Pro Ile Ala Leu Asn Trp Thr Leu Leu Asn Val Ser Leu
    150                 155                 160

act ggg att cat gca gat atc caa gtg aga tgg gaa gca cca cgc aat     583
Thr Gly Ile His Ala Asp Ile Gln Val Arg Trp Glu Ala Pro Arg Asn
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165                 170                 175                 180

gca gat att cag aaa gga tgg atg gtt ctg gag tat gaa ctt caa tac     631
Ala Asp Ile Gln Lys Gly Trp Met Val Leu Glu Tyr Glu Leu Gln Tyr
                185                 190                 195

aaa gaa gta aat gaa act aaa tgg aaa atg atg gac cct ata ttg aca     679
Lys Glu Val Asn Glu Thr Lys Trp Lys Met Met Asp Pro Ile Leu Thr
            200                 205                 210

aca tca gtt cca gtg tac tca ttg aaa gtg gat aag gaa tat gaa gtg     727
Thr Ser Val Pro Val Tyr Ser Leu Lys Val Asp Lys Glu Tyr Glu Val
        215                 220                 225

cgt gtg aga tcc aaa caa cga aac tct gga aat tat ggc gag ttc agt     775
Arg Val Arg Ser Lys Gln Arg Asn Ser Gly Asn Tyr Gly Glu Phe Ser
    230                 235                 240

gag gtg ctc tat gta aca ctt cct cag atg agc caa ttt aca tgt gaa     823
Glu Val Leu Tyr Val Thr Leu Pro Gln Met Ser Gln Phe Thr Cys Glu
245                 250                 255                 260

gaa gat ttc tac ttt cca tgg ctc tta att att atc ttt gga ata ttt     871
Glu Asp Phe Tyr Phe Pro Trp Leu Leu Ile Ile Ile Phe Gly Ile Phe
                265                 270                 275

ggg cta aca gtg atg cta ttt gta ttc tta ttt tct aaa cag caa agg     919
Gly Leu Thr Val Met Leu Phe Val Phe Leu Phe Ser Lys Gln Gln Arg
            280                 285                 290

att aaa atg ctg att ctg ccc cca gtt cca gtt cca aag att aaa gga     967
Ile Lys Met Leu Ile Leu Pro Pro Val Pro Val Pro Lys Ile Lys Gly
        295                 300                 305

atc gat cca gat ctc ctc aag gaa gga aaa tta gag gag gtg aac aca    1015
Ile Asp Pro Asp Leu Leu Lys Glu Gly Lys Leu Glu Glu Val Asn Thr
    310                 315                 320

atc tta gcc att cat gat agc tat aaa ccc gaa ttc cac agt gat gac    1063
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Ile Leu Ala Ile His Asp Ser Tyr Lys Pro Glu Phe His Ser Asp Asp
325                 330                 335                 340

tct tgg gtt gaa ttt att gag cta gat att gat gag cca gat gaa aag    1111
Ser Trp Val Glu Phe Ile Glu Leu Asp Ile Asp Glu Pro Asp Glu Lys
                345                 350                 355

act gag gaa tca gac aca gac aga ctt cta agc agt gac cat gag aaa    1159
Thr Glu Glu Ser Asp Thr Asp Arg Leu Leu Ser Ser Asp His Glu Lys
            360                 365                 370

tca cat agt aac cta ggg gtg aag gat ggc gac tct gga cgt acc agc    1207
Ser His Ser Asn Leu Gly Val Lys Asp Gly Asp Ser Gly Arg Thr Ser
        375                 380                 385

tgt tgt gaa cct gac att ctg gag act gat ttc aat gcc aat gac ata    1255
Cys Cys Glu Pro Asp Ile Leu Glu Thr Asp Phe Asn Ala Asn Asp Ile
    390                 395                 400

cat gag ggt acc tca gag gtt gct cag cca cag agg tta aaa ggg gaa    1303
His Glu Gly Thr Ser Glu Val Ala Gln Pro Gln Arg Leu Lys Gly Glu
405                 410                 415                 420

gca gat ctc tta tgc ctt gac cag aag aat caa aat aac tca cct tat    1351
Ala Asp Leu Leu Cys Leu Asp Gln Lys Asn Gln Asn Asn Ser Pro Tyr
                425                 430                 435

cat gat gct tgc cct gct act cag cag ccc agt gtt atc caa gca gag    1399
His Asp Ala Cys Pro Ala Thr Gln Gln Pro Ser Val Ile Gln Ala Glu
            440                 445                 450

aaa aac aaa cca caa cca ctt cct act gaa gga gct gag tca act cac    1447
Lys Asn Lys Pro Gln Pro Leu Pro Thr Glu Gly Ala Glu Ser Thr His
        455                 460                 465

caa gct gcc cat att cag cta agc aat cca agt tca ctg tca aac atc    1495
Gln Ala Ala His Ile Gln Leu Ser Asn Pro Ser Ser Leu Ser Asn Ile
    470                 475                 480
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gac ttt tat gcc cag gtg agc gac att aca cca gca ggt agt gtg gtc    1543
Asp Phe Tyr Ala Gln Val Ser Asp Ile Thr Pro Ala Gly Ser Val Val
485                 490                 495                 500

ctt tcc ccg ggc caa aag aat aag gca ggg atg tcc caa tgt gac atg    1591
Leu Ser Pro Gly Gln Lys Asn Lys Ala Gly Met Ser Gln Cys Asp Met
                505                 510                 515

cac ccg gaa atg gtc tca ctc tgc caa gaa aac ttc ctt atg gac aat    1639
His Pro Glu Met Val Ser Leu Cys Gln Glu Asn Phe Leu Met Asp Asn
            520                 525                 530

gcc tac ttc tgt gag gca gat gcc aaa aag tgc atc cct gtg gct cct    1687
Ala Tyr Phe Cys Glu Ala Asp Ala Lys Lys Cys Ile Pro Val Ala Pro
        535                 540                 545

cac atc aag gtt gaa tca cac ata cag cca agc tta aac caa gag gac    1735
His Ile Lys Val Glu Ser His Ile Gln Pro Ser Leu Asn Gln Glu Asp
    550                 555                 560

att tac atc acc aca gaa agc ctt acc act gct gct ggg agg cct ggg    1783
Ile Tyr Ile Thr Thr Glu Ser Leu Thr Thr Ala Ala Gly Arg Pro Gly
565                 570                 575                 580

aca gga gaa cat gtt cca ggt tct gag atg cct gtc cca gac tat acc    1831
Thr Gly Glu His Val Pro Gly Ser Glu Met Pro Val Pro Asp Tyr Thr
                585                 590                 595

tcc att cat ata gta cag tcc cca cag ggc ctc ata ctc aat gcg act    1879
Ser Ile His Ile Val Gln Ser Pro Gln Gly Leu Ile Leu Asn Ala Thr
            600                 605                 610

gcc ttg ccc ttg cct gac aaa gag ttt ctc tca tca tgt ggc tat gtg    1927
Ala Leu Pro Leu Pro Asp Lys Glu Phe Leu Ser Ser Cys Gly Tyr Val
        615                 620                 625

agc aca gac caa ctg aac aaa atc atg cct tag cctttctttg gtttcccaag  1980
Ser Thr Asp Gln Leu Asn Lys Ile Met Pro
    630                 635
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ttaaaccttt tttgggggag tgacaggatg gggtatggat tctaaaatgc cttttcccaa 2100

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aaaaaactaa aaactagagg tgagaaattt aaactataag caagaaggca aaaatagttt 2460

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ccggcagccg cggggatccc gggctgggtc cacgcggcct gaggcctcgg ctccagcagc 180

ccccaagcgg acacgaaccc gcgttctgtc tcccgaggcg aaactccgag gtctcaggt 239

atg gat ctt tgt cag gtc ttc tta acc ttg gca ctg gca gtc acc agc 287
Met Asp Leu Cys Gln Val Phe Leu Thr Leu Ala Leu Ala Val Thr Ser
1 5 10 15

agc aca ttt tct gga agt gag gct aca cca gct act ctt ggc aaa gct 335
Ser Thr Phe Ser Gly Ser Glu Ala Thr Pro Ala Thr Leu Gly Lys Ala
20 25 30

tcc cca gtt ctg caa aga atc aat cca agc ctg ggg aca agt tct tct 383

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Ser Pro Val Leu Gln Arg Ile Asn Pro Ser Leu Gly Thr Ser Ser Ser
         35                  40                  45

gga aag cct cga ttc acc aag tgt cgt tcc cct gaa ctg gag aca ttt     431
Gly Lys Pro Arg Phe Thr Lys Cys Arg Ser Pro Glu Leu Glu Thr Phe
     50                  55                  60

tca tgc tac tgg aca gaa gga gat aat cct gat tta aag acc cca gga     479
Ser Cys Tyr Trp Thr Glu Gly Asp Asn Pro Asp Leu Lys Thr Pro Gly
 65                  70                  75                  80

tct att cag ctg tac tat gct aaa agg gaa agc caa cga caa gct gca     527
Ser Ile Gln Leu Tyr Tyr Ala Lys Arg Glu Ser Gln Arg Gln Ala Ala
                85                  90                  95

aga att gct cat gaa tgg acc cag gaa tgg aaa gaa tgc cct gat tat     575
Arg Ile Ala His Glu Trp Thr Gln Glu Trp Lys Glu Cys Pro Asp Tyr
            100                 105                 110

gtc tct gct gga aaa aac agc tgt tac ttc aac tca tca tat acc tcc     623
Val Ser Ala Gly Lys Asn Ser Cys Tyr Phe Asn Ser Ser Tyr Thr Ser
        115                 120                 125

att tgg ata ccc tac tgc atc aag cta act aca aat ggt gat ttg ctg     671
Ile Trp Ile Pro Tyr Cys Ile Lys Leu Thr Thr Asn Gly Asp Leu Leu
    130                 135                 140

gac caa aaa tgt ttc act gtt gac gaa ata gtg caa cct gat cca ccc     719
Asp Gln Lys Cys Phe Thr Val Asp Glu Ile Val Gln Pro Asp Pro Pro
145                 150                 155                 160

att ggc ctc aac tgg act tta cta aac att agt ttg acc ggg att cgt     767
Ile Gly Leu Asn Trp Thr Leu Leu Asn Ile Ser Leu Thr Gly Ile Arg
                165                 170                 175

gga gac atc caa gtg agt tgg caa cca cca ccc aat gca gat gtt ctg     815
Gly Asp Ile Gln Val Ser Trp Gln Pro Pro Pro Asn Ala Asp Val Leu
            180                 185                 190
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aag gga tgg ata att ctg gag tat gaa att cag tac aaa gaa gta aat     863
Lys Gly Trp Ile Ile Leu Glu Tyr Glu Ile Gln Tyr Lys Glu Val Asn
        195                 200                 205

gaa tca aaa tgg aaa gtg atg ggc cct ata tgg tta aca tac tgt cca     911
Glu Ser Lys Trp Lys Val Met Gly Pro Ile Trp Leu Thr Tyr Cys Pro
    210                 215                 220

gtg tac tca ttg aga atg gat aaa gaa cat gaa gtg cgg gtg aga tcc     959
Val Tyr Ser Leu Arg Met Asp Lys Glu His Glu Val Arg Val Arg Ser
225                 230                 235                 240

aga caa cgg agc ttt gaa aag tac agc gag ttc agc gaa gtc ctc cgt    1007
Arg Gln Arg Ser Phe Glu Lys Tyr Ser Glu Phe Ser Glu Val Leu Arg
                245                 250                 255

gta ata ttt cct cag acg aac ata ttg gaa gca tgt gaa gaa gat atc    1055
Val Ile Phe Pro Gln Thr Asn Ile Leu Glu Ala Cys Glu Glu Asp Ile
            260                 265                 270

cag ttt cca tgg ttc tta att att atc ttt gga ata ttt gga gta gca    1103
Gln Phe Pro Trp Phe Leu Ile Ile Ile Phe Gly Ile Phe Gly Val Ala
        275                 280                 285

gtg atg cta ttt gta gtt ata ttt tca aag cag caa agg att aag atg    1151
Val Met Leu Phe Val Val Ile Phe Ser Lys Gln Gln Arg Ile Lys Met
    290                 295                 300

ctg att tta ccc cca gtc cca gtt cca aag att aaa ggg att gat cca    1199
Leu Ile Leu Pro Pro Val Pro Val Pro Lys Ile Lys Gly Ile Asp Pro
305                 310                 315                 320

gat ctt ctc aag gga ggg aag ttg gag gag gtg aac acc atc tta ggc    1247
Asp Leu Leu Lys Gly Gly Lys Leu Glu Glu Val Asn Thr Ile Leu Gly
                325                 330                 335

att cat gat aac tac aaa ccc gac ttc tac aat gat gat tcc tgg gtc    1295
Ile His Asp Asn Tyr Lys Pro Asp Phe Tyr Asn Asp Asp Ser Trp Val
            340                 345                 350
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gag ttc att gag cta gat att gat gaa gca gat gtg gat gag aag act    1343
Glu Phe Ile Glu Leu Asp Ile Asp Glu Ala Asp Val Asp Glu Lys Thr
        355                 360                 365

gaa ggg tct gac aca gac aga ctt cta agc aat gat cat gag aaa tca    1391
Glu Gly Ser Asp Thr Asp Arg Leu Leu Ser Asn Asp His Glu Lys Ser
    370                 375                 380

gct ggt atc ctt gga gca aag gat gat gat tct ggg cgt acc agc tgt    1439
Ala Gly Ile Leu Gly Ala Lys Asp Asp Asp Ser Gly Arg Thr Ser Cys
385                 390                 395                 400

tac gac cct gac att ttg gat act gat ttc cat acc agt gac atg tgt    1487
Tyr Asp Pro Asp Ile Leu Asp Thr Asp Phe His Thr Ser Asp Met Cys
                405                 410                 415

gat ggt acc ttg aag ttt gct cag tca cag aag tta aat atg gaa gct    1535
Asp Gly Thr Leu Lys Phe Ala Gln Ser Gln Lys Leu Asn Met Glu Ala
            420                 425                 430

gat ctc ttg tgc ctt gat cag aag aat ctg aag aac ttg cct tat gat    1583
Asp Leu Leu Cys Leu Asp Gln Lys Asn Leu Lys Asn Leu Pro Tyr Asp
        435                 440                 445

gct tcc ctt ggc tct ctg cat ccc tcc att acc cag aca gta gaa gaa    1631
Ala Ser Leu Gly Ser Leu His Pro Ser Ile Thr Gln Thr Val Glu Glu
    450                 455                 460

aac aag cca cag cca ctt ttg agc agc gaa act gag gca acc cac caa    1679
Asn Lys Pro Gln Pro Leu Leu Ser Ser Glu Thr Glu Ala Thr His Gln
465                 470                 475                 480

ctc gcc tct aca ccg atg agt aat ccc aca tca ctg gca aac att gac    1727
Leu Ala Ser Thr Pro Met Ser Asn Pro Thr Ser Leu Ala Asn Ile Asp
                485                 490                 495

ttt tat gcc caa gta agc gac att aca cca gca ggt ggt gat gtc ctt    1775
Phe Tyr Ala Gln Val Ser Asp Ile Thr Pro Ala Gly Gly Asp Val Leu
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            500                 505                 510

tcc cca ggc caa aag att aag gca ggg ata gcc caa ggc aat acc cag    1823
Ser Pro Gly Gln Lys Ile Lys Ala Gly Ile Ala Gln Gly Asn Thr Gln
        515                 520                 525

cgg gag gtg gcc acg ccc tgc caa gaa aat tac agc atg aac agt gcc    1871
Arg Glu Val Ala Thr Pro Cys Gln Glu Asn Tyr Ser Met Asn Ser Ala
    530                 535                 540

tac ttt tgt gag tca gat gcc aaa aaa tgc atc gct gtg gcc cgt cgc    1919
Tyr Phe Cys Glu Ser Asp Ala Lys Lys Cys Ile Ala Val Ala Arg Arg
545                 550                 555                 560

atg gaa gcc acg tct tgt ata aaa cca agc ttt aac caa gag gac att    1967
Met Glu Ala Thr Ser Cys Ile Lys Pro Ser Phe Asn Gln Glu Asp Ile
                565                 570                 575

tac atc acc aca gaa agc ctt acc act act gcc cag atg tct gag aca    2015
Tyr Ile Thr Thr Glu Ser Leu Thr Thr Thr Ala Gln Met Ser Glu Thr
            580                 585                 590

gca gat att gct cca gat gct gag atg tct gtc cca gac tac acc acg    2063
Ala Asp Ile Ala Pro Asp Ala Glu Met Ser Val Pro Asp Tyr Thr Thr
        595                 600                 605

gtt cac acc gtg cag tct cca agg ggc ctt ata ctc aac gca act gct    2111
Val His Thr Val Gln Ser Pro Arg Gly Leu Ile Leu Asn Ala Thr Ala
    610                 615                 620

ttg cct ttg cct gac aaa aag aat ttt ccc tcc tcg tgt ggt tat gtg    2159
Leu Pro Leu Pro Asp Lys Lys Asn Phe Pro Ser Ser Cys Gly Tyr Val
625                 630                 635                 640

agc aca gac caa ctg aac aaa atc atg cag tag cctttcctat ctttaaatgg  2212
Ser Thr Asp Gln Leu Asn Lys Ile Met Gln
                645                 650

caagggaaag gctgggcaca aacgcttaaa ccaaaactat gttttaaatc tgtgttggga  2272
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